

SEQUENCE ALIGNMENT

1#

FT	VARSP LIC	1143	1203	WGASSSLPQSPARVTTSMVTVAHPPLPLPGAYIHAPPEPPW
FT	FT			SPATSSGNTSSRGKPGPATG -> PEEI (in isoform 2).
FT	FT			/FTid=VSP_004542.
FT	VARIANT	346	346	E -> Q.
FT	VARIANT	493	493	/FTid=VAR_018935.
FT	VARIANT	622	622	E -> K.
FT	VARIANT	988	988	/FTid=VAR_018936.
FT	VARIANT	1019	1019	H -> Y.
FT	VARIANT	1121	1121	/FTid=VAR_018937.
FT	VARIANT	1019	1019	T -> M.
FT	VARIANT	1121	1121	/FTid=VAR_018938.
FT	VARIANT	1121	1121	V -> M.
FT	VARIANT	1121	1121	/FTid=VAR_018939.
FT	VARIANT	1121	1121	I -> M.
FT	VARIANT	1121	1121	/FTid=VAR_018940.
FT	VARIANT	120	120	T -> N (in Ref. 2).
FT	VARIANT	120	120	R -> L (in Ref. 2).
FT	VARIANT	175	175	Q -> W (in Ref. 1).
FT	VARIANT	753	753	Q -> R (in Ref. 2).
FT	VARIANT	787	787	N -> S (in Ref. 2).
FT	VARIANT	833	833	P -> L (in Ref. 2).
FT	VARIANT	837	837	S -> G (in Ref. 2).
FT	VARIANT	846	846	D -> E (in Ref. 2).
FT	VARIANT	897	897	L -> F (in Ref. 3).
FT	VARIANT	1203	1203	AA: 130543 MW; 4FAB06999782C031_CRC64;
FT	SEQUENCE	1203	AA: 130543 MW; 4FAB06999782C031_CRC64;	
Qy	Query Match	99.8%;	Score 4258; DB 1; Length 1203;	
Qy	Best Local Similarity	99.9%;	Pred. No. 0;	
Qy	Matches 1202; Conservative	0; Mismatches	1; Indels 0; Gaps 0;	
Qy	1	MTRSPPLRELPPPTTPPARTAPQILAGSLKAPLMRAYFQGLLPSLGGCIGORHCNKLP	60	
Db	1	MTRSPPLRELPPPTTPPARTAPQILAGSLKAPLMRAYFQGLLPSLGGCIGORHCNKLP	60	
Qy	61	LGLLAFGALALGLRWIIETNMLBOLWVEGSRVSQELHYTKEKGEEAAYTSQMLQTAR	120	
Db	61	LGLLAFGALALGLRWIETNLEOLWVEGSRVSQELHYTKEKGEEAAYTSQMLQTAR	120	
Qy	121	QEGENILTPREALGLQALATASKVQVSLYSGKSWDLNKICYKSGVPLIENGMIEMIEKL	180	
Db	121	QEGENILTPREALGLHLQALATASKVQVSLYSGKSWDLNKICYKSGVPLIENGMIEMIEKL	180	
Qy	181	FPCCVILTPDCEMEGAKLQGSYLPGRDPIQWNLDPQOLLEELGPFASLEGFRELDDK	240	
Db	181	FPCCVILTPDCEMEGAKLQGSATLPGRDPIQWNLDPQOLLEELGPFASLEGFRELDDK	240	
Qy	241	AQVGQAYVGRPCILHPDDDLHCPSPAPNHRSQAPNVAHELSCGCHGFSGHKPMHQEELLG	300	
Db	241	AQVGQAYVGRPCILHPDDDLHCPSPAPNHRSQAPNVAHELSCGCHGFSGHKPMHQEELLG	300	
Qy	301	GNARDPQCELLRAEALQSTFLLKSPROLYNHFGRGYQTHDLGWSEEQASTVLQAWORRV	360	
Db	301	GNARDPQCELLRAEALQSTFLLKSPROLYNHFGRGYQTHDLGWSEEQASTVLQAWORRV	360	
Qy	361	QLAQEALPENASQOIHAFPSSTLDDILHAFSSVARNVGGYGLMLAYACVTLMLWDCAQ	420	
Db	361	QLAQEALPENASQOIHAFPSSTLDDILHAFSSVARNVGGYGLMLAYACVTLMLWDCAQ	420	
Qy	421	SQSGVGLAGVLVALVASGLGICALLGITFNAATQVLPFLALGIGVDVFLAHAFTE	480	
Db	421	SQSGVGLAGVLVALVASGLGICALLGITFNAATQVLPFLALGIGVDVFLAHAFTE	480	
Qy	481	ALPGTPLQERMGECIQRTGTSVVLTSINNMAFLMAALVPTALRAFSLQAAITWGCITFV	540	
Db	481	ALPGTPLQERMGECIQRTGTSVVLTSINNMAFLMAALVPTALRAFSLQAAITWGCITFV	540	
Qy	541	AWNLVPPATLSLDIRRRHCORLDVLCFFSSPSCAQVIQILPQELGQGVPGVIAHLTATV	600	
Db	541	AWNLVPPATLSLDIRRRHCORLDVLCFFSSPSCAQVIQILPQELGQGVPGVIAHLTATV	600	
Qy	601	QAPTHCEASSQHVVTILPPQANLVPPSPDPLGSELFSFGSTRLDLCQERTKQAKCS	660	

601	QAFTHCEASSQHVVTILPPOAHVLVPPSPDPLGSELSPFGSGTRDLLGQEBETRQKAACKS	660
661	LPCARNWLAHFAFYQAPAPLLQSHAKAIVLVLFAGALLGLSLYGATLVQDGLATDPVPRG	720
665	LPCARNWLAHFAFYQAPAPLLQSHAKAIVLVLFAGALLGLSLYGATLVQDGLATDPVPRG	720
721	TKRHAFLSAQLRYSFSLYEVALVTQGGFDYAHQSORALFDLHORFSSLKAVLPPPTAQAPRT	780
721	TKRHAFLSAQLRYSFSLYEVALVTQGGFDYAHQSORALFDLHORFSSLKAVLPPPTAQAPRT	780
781	WLHYRWNWLOQIAAFQDDQWASGRITRHSYRNGSBDGALAYKLLIQTGDAQEPDLSQLT	840
781	WLHYRWNWLOQIAAFQDDQWASGRITRHSYRNGSBDGALAYKLLIQTGDAQEPDLSQLT	840
841	TRKLVDRREGILPPELFYMLTVMWSSDPLGLAASQANFYPPPPMLHDKYDTTGENLRIP	900
841	TRKLVDRREGILPPELFYMLTVMWSSDPLGLAASQANFYPPPPMLHDKYDTTGENLRIP	900
901	PAQPLEFAQPFLLRGLOKTADEYENEGARNACACAGQACVHAPSGSPFLFWEQYVGL	960
901	PAQPLEFAQPFLLRGLOKTADEYENEGARNACACAGQACVHAPSGSPFLFWEQYVGL	960
961	RCFLLAVCILLVCTFLVCAILLNFWTAGTIVLANMTVELFGIMFGIKLSAIPV	1020
961	RCFLLAVCILLVCTFLVCAILLNFWTAGTIVLANMTVELFGIMFGIKLSAIPV	1020
1021	ILVASGVGVEFTVHVALGFLTITQGSRLRAHALEHTFAPDTGATSLTLLGLMAGSH	1080
1021	ILVASGVGVEFTVHVALGFLTITQGSRLRAHALEHTFAPDTGATSLTLLGLMAGSH	1080
1081	PDFIVRVFFPAALTIVLLGLLHGLVLLPVLLSLGPPPEVIMYKESPELSPAPQGGG	1140
1081	PDFIVRVFFPAALTIVLLGLLHGLVLLPVLLSLGPPPEVIMYKESPELSPAPQGGG	1140
1141	LRWGASSSLPQSFAVTTSMVAIHPPPLPGAYIHPAPDPSPMSPAAATSSGNLSRSGPGP	1200
1141	LRWGASSSLPQSFAVTTSMVAIHPPPLPGAYIHPAPDPSPMSPAAATSSGNLSRSGPGP	1200
1201	ATG 1203	
1201	ATG 1203	
RESULT 5		
PTC2 MOUSE		
ID	PTC2 MOUSE	STANDARD; PRT: 1182 AA.
AC	O35595;	
DT	30-MAY-2000 (Rel. 39, Created)	
DT	30-MAY-2000 (Rel. 39, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DE	Patched protein homolog 2 (PTC2).	
GN	Name=Ptch2;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
NCBI	TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RP	TISSUE=Embryo;	
RC	MEDLINE=98132566; PubMed=94627314;	
RC	MoCoyama J., Takabatake T., Takehima K., Hui C.-C.;	
RA	"Ptch2, a second mouse patched gene is co-expressed with Sonic	
RT	hedghog",	
RT	Nat. Genet. 18:104-106(1998).	
RN	[2]	
RP	SEQUENCE OF 196-446 FROM N.A.	
RC	STRAIN=BALB/c; TISSUE=Neuroretina;	
RC	MEDLINE=37379366; PubMed=9237688;	
RA	Takabatake T., Ogawa M., Takahashi T.C., Mizuno M., Okamoto M.,	
RT	Takehima K.;	
RT	"Hedgehog and patched gene expression in adult ocular tissues.";	
RT	FEBS Lett. 410:485-489(1997).	
CC	is FUNCTION. May have a role in ocular development. Mus.	

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)